

# EXHIBIT 1

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Clustalw2--HTX18 pat seqa.txt

Results of search  
 Number of sequences11  
 Alignment score64595  
 Sequence formatPearson  
 Sequence typeaa  
 Jalview  
 Output fileclustalw2-20080418-16010091.output  
 Alignment fileclustalw2-20080418-16010091.a1n  
 Guide tree fileclustalw2-20080418-16010091.dnd  
 Your input fileclustalw2-20080418-16010091.input

To save a result file right-click the file link in the above table and choose "Save Target As".  
 If you cannot see the Jalview button, reload the page and check your browser settings to enable Java Applets.

#### Scores Table

Length		Alignment Score		Sequence Number		Sequence Name		Sequence	
SeqA	Name	Len(aa)	SeqB	Name	Len(aa)	Score			
1	Trx	190	2	TPX116G	190	99			
1	Trx	190	3	TPX118C	190	99			
1	Trx	190	4	TPXHMLAHAE144R	190	95			
1	Trx	190	5	TPXHMLAHAE144R161R	190	95			
1	Trx	190	6	TPXHMLAHAE116G144R	190	95			
1	Trx	190	7	TPXHMLAHAE118C144R	190	95			
1	Trx	190	8	TPXH1DMLAHAE144R161R	190	94			
1	Trx	190	9	TPXH1DMLAHAE116G144R161R	190	94			
1	Trx	190	10	TPXH1DMLAHAE118C144R161R	190	94			
1	Trx	190	11	TPXH1DMLAHAE116G118C144R161R	190	93			
2	Trx116G	190	3	Trx118C	190	98			
2	Trx116G	190	4	TPXHMLAHAE144R	190	95			
2	Trx116G	190	5	TPXHMLAHAE144R161R	190	94			
2	Trx116G	190	6	TPXHMLAHAE116G144R	190	95			
2	Trx116G	190	7	TPXHMLAHAE118C144R	190	94			
2	Trx116G	190	8	TPXH1DMLAHAE144R161R	190	94			
2	Trx116G	190	9	TPXH1DMLAHAE116G144R161R	190	94			
2	Trx116G	190	10	TPXH1DMLAHAE118C144R161R	190	93			
2	Trx116G	190	11	TPXH1DMLAHAE116G118C144R161R	190	94			
3	Trx118C	190	4	TPXHMLAHAE144R	190	95			
3	Trx118C	190	5	TPXHMLAHAE144R161R	190	94			
3	Trx118C	190	6	TPXHMLAHAE116G144R	190	94			
3	Trx118C	190	7	TPXHMLAHAE118C144R	190	95			
3	Trx118C	190	8	TPXH1DMLAHAE144R161R	190	94			
3	Trx118C	190	9	TPXH1DMLAHAE116G144R161R	190	93			
3	Trx118C	190	10	TPXH1DMLAHAE118C144R161R	190	94			
3	Trx118C	190	11	TPXH1DMLAHAE116G118C144R161R	190	94			
4	TPXHMLAHAE144R	190	5	TPXHMLAHAE144R161R	190	99			
4	TPXHMLAHAE144R	190	6	TPXHMLAHAE116G144R	190	99			
4	TPXHMLAHAE144R	190	7	TPXHMLAHAE118C144R	190	99			
4	TPXHMLAHAE144R	190	8	TPXH1DMLAHAE144R161R	190	98			
4	TPXHMLAHAE144R	190	9	TPXH1DMLAHAE116G144R161R	190	98			
4	TPXHMLAHAE144R	190	10	TPXH1DMLAHAE118C144R161R	190	98			
4	TPXHMLAHAE144R	190	11	TPXH1DMLAHAE116G118C144R161R	190	97			
5	TPXHMLAHAE116G144R	190	6	TPXHMLAHAE116G144R	190	98			
5	TPXHMLAHAE144R161R	190	7	TPXHMLAHAE118C144R	190	98			
5	TPXHMLAHAE144R161R	190	8	TPXH1DMLAHAE144R161R	190	99			

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5	TrxHMLAHAE144R161R	190	9
5	TrxHMLAHAE144R161R	190	10
5	TrxHMLAHAE144R161R	190	11
6	TrxHMLAHAE116G144R	190	7
6	TrxHMLAHAE116G144R	190	8
6	TrxHMLAHAE116G144R	190	9
6	TrxHMLAHAE116G144R	190	10
6	TrxHMLAHAE116G144R	190	11
7	TrxHMLAHAE118C144R	190	8
7	TrxHMLAHAE118C144R	190	9
7	TrxHMLAHAE118C144R	190	10
7	TrxHMLAHAE118C144R	190	11
8	TrxH11DMLAHAE144R161R	190	9
8	TrxH11DMLAHAE144R161R	190	10
7	TrxH11DMLAHAE144R161R	190	11
9	TrxH11DMLAHAE116G144R161R	190	10
9	TrxH11DMLAHAE116G144R161R	190	11
10	TrxH11DMLAHAE118C144R161R	190	11

NOTE: Some scores may be missing from the above table if the  
alignment was done using multiple CPU mode. Please check the output.

Length	Alignment Score	Sequence Number	Sequence Name	Sequence		
Alignment						
CLUSTAL 2.0.5 multiple sequence alignment						
TrxHMLAHAE144R		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
TrxHMLAHAE116G144R		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
TrxH11DMLAHAE116G144R161R		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
TrxH11DMLAHAE116G118C144R161R		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
TrxH11DMLAHAE118C144R161R		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
TrxH11DMLAHAE144R161R		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
TrxHMLAHAE118C144R		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
Trx		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
TrxL16G		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
TrxL118C		QTIQPGTG	YHNGYFYSY	NDGHGGVTMTLPGGGQFSVNWNSNGNFVGGGK 50		
				*****::***** * *****		
TrxHMLAHAE144R		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxHMLAHAE116G144R		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxH11DMLAHAE116G144R161R		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxH11DMLAHAE116G118C144R161R		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxH11DMLAHAE118C144R161R		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxH11DMLAHAE144R161R		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxHMLAHAE144R161R		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxHMLAHAE118C144R		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
Trx		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxL16G		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
TrxL118C		WPGTKKNK	VINFGSGYNPNNGSYL	AVYGWSRNP	LIYYI	VENFGTYNPST 100
				*****::***** * *****		

TrxHMLAHAE144R	GATKHGEVTSDGS	YDIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
TrxHMLAHAE116G144R	GATKHGEVTSDGS	YGIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
TrxH11DMLAHAE116G144R161R	GATKHGEVTSDGS	YGIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
TrxH11DMLAHAE116G118C144R161R	GATKHGEVTSDGS	YGIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
TrxH11DMLAHAE118C144R161R	GATKHGEVTSDGS	YDIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
TrxHMLAHAE144R161R	GATKHGEVTSDGS	YDIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
TrxHMLAHAE118C144R	GATKHGEVTSDGS	YDIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
Trx	GATKHGEVTSDGS	YDIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
TrxL16G	GATKHGEVTSDGS	YGIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
TrxL18C	GATKHGEVTSDGS	YDIYRTQRVNAPS	IEGTATFYQYWSVRNRRSSGVS 150
*** ***** * *****			
TrxHMLAHAE144R	NTANHFN	AWAQOGLT	GMTDYGIVAVEGFSSGSASITVS 190
TrxHMLAHAE116G144R	NTANHFN	AWAQOGLT	GMTDYGIVAVEGFSSGSASITVS 190
TrxH11DMLAHAE116G144R161R	NTANHFN	AWAQOGLT	GMTDYGIVAVEGFSSGSASITVS 190
TrxH11DMLAHAE116G118C144R161R	NTANHFN	AWAQOGLT	GMTDYGIVAVEGFSSGSASITVS 190
TrxH11DMLAHAE144R161R	NTANHFN	AWAQOGLT	GMTDYGIVAVEGFSSGSASITVS 190
TrxH11DMLAHAE118C144R161R	NTANHFN	AWAQOGLT	GMTDYGIVAVEGFSSGSASITVS 190

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Clustalw2--HTX18 pat seqa.txt
TrxHMLAHAE144R161R      NTANHFNAWAQQLTLGTMDYQIVAVEGYFSSGASITVS 190
TrxHMLAHAE118C144R      NTANHFNAWAQQLTLGTMDYQIVAVEGYFSSGASITVS 190
Trx                      NTANHFNAWAQQLTLGTMDYQIVAVEGYFSSGASITVS 190
Trx1116G                 NTANHFNAWAQQLTLGTMDYQIVAVEGYFSSGASITVS 190
Trx1118C                 NTANHFNAWAQQLTLGTMDYQIVAVEGYFSSGASITVS 190

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PLEASE NOTE: Showing colors on large alignments is slow.

#### Guide Tree

```

(
(
(
Trx:0.00175,
Trx116G:0.00351)
:0.00099,
Trx118C:0.00428)
:0.03914,
TrxHMLAHAE118C144R:0.00296)
:0.00181,
(
TrxHMLAHAE144R161R:0.00115,
(
TrxH11DMLAHAE144R161R:0.00184,
(
TrxH11DMLAHAE116G144R161R:0.00188,
TrxH11DMLAHAE116G118C144R161R:0.00338)
:0.00219,
TrxH11DMLAHAE118C144R161R:0.00307)
:0.00079)
:0.00411)
:0.00444)
:0.00016,
TrxHMLAHAE144R:0.00066,
TrxHMLAHAE116G144R:0.00461);

```

#### Cladogram

Right-click on the above tree to see display options.  
Problems printing? Read how to print a Phylogram or Cladogram.